

SEQUENCE LISTING

<110> Liao et al.

<120> ALANINE 2,3-AMINOMUTASE

<130> 63358-09

<150> PCT/US03/01635

<151> 2003-01-17

<150> US 60/350,727

<151> 2002-01-18

<150> US 60/375,785

<151> 2002-04-25

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

gcgcgaggag gagttcatat gaaaaacaaa tggataaac

40

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<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 2

cgggcaccgc ttcgaggcgg ccgcaccatt cgcattg

36

<210> 3

<211> 1416

<212> DNA

<213> Bacillus subtilis

<400> 3

ttgaaaaaca aatggtataa accgaaacgg cattggaagg agatcgagtt atggaaggac

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gttcggaag agaaatggaa cgattggctt tggcagctga cacacactgt aagaacgtta

120

gatgatttaa agaaagtc	taatctgacc	gaggatgaag	aggaaggcgt	cagaatttct	180
acaaaaacga tccccttaa	tattacacct	tactatgctt	ctttaatgga	ccccgacaat	240
ccgagatgcc cggtagcat	gcagtctgtg	ccgctttctg	aagaaatgca	caaaacaaaa	300
tacgatctgg aagaccgct	tcatgaggat	gaagattcac	cggtagccgg	tctgacacac	360
cgctatcccg accgtgtgt	gtttcttgtc	acgaatcaat	gttccatgta	ctgccgctac	420
tgcacaagaa ggcgttttc	cggacaaatc	ggaatgggcg	tccccaaaaa	acagcttgat	480
gctgcaattg cttatatccg	ggaaacaccc	gaaatccgcg	attgtttaat	ttcaggcggt	540
gatgggctgc tcatcaacga	ccaaatttta	gaatatat	ttaaagagct	gcgcagcatt	600
ccgcatctgg aagtcacag	aatcggaaca	agagctcccg	tcgtctttcc	gcagcgcat	660
accgatcatc tgtgcgagat	attgaaaaaa	tatcatccgg	tctggctgaa	caccattttt	720
aacacaagca tcgaaatgac	agaagaatcc	gttgaggcat	gtgaaaagct	ggtgaacgcg	780
ggagtgccgg tcggaaatca	ggctgtcgta	ttagcaggta	ttaatgattc	ggttccaatt	840
atgaaaaagc tcatgcatga	cttggtaaaa	atcagagtcc	gtccttatta	tatttaccaa	900
tgtgatctgt cagaaggaat	agggcatttc	agagctcctg	tttccaaagg	tttggagatc	960
attgaagggc tgagagggtca	tacctcaggc	tatgcgggtc	ctacctttgt	cgttgacgca	1020
ccaggcggag gaggtaaaat	cgccctgcag	ccaaactatg	tcctgtcaca	aagtctcgac	1080
aaagtgatct taagaaattt	tgaagggtgtg	attacgtcat	atccggaacc	agagaattat	1140
atccccaatc aggcagacgc	ctattttgag	tccgttttcc	ctgaaaccgc	tgacaaaaag	1200
gagccgatcg ggctgagtgc	catttttgct	gacaaagaag	tttcgtttac	acctgaaaat	1260
gtagacagaa tcaaaaggag	agaggcatac	atcgcaaatc	cggagcatga	aacattaaaa	1320
gatcggcgtg agaaaagaga	tcagctcaaa	gaaaagaaat	ttttggcgca	gcagaaaaaa	1380
cagaaagaga ctgaatgcgg	aggggattct	tcatga			1416

<210> 4
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<220>
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gtgtaggctg	gagctgcttc
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<210> 5
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 5
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 <210> 6
 <211> 20
 <212> DNA
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 <220>
 <223> PCR primer

 <400> 6
 ttaccgagca gcgttcagag 20

 <210> 7
 <211> 20
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 <220>
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 <400> 7
 cacctggcgg tgacaaccat 20

 <210> 8
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

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 <212> DNA
 <213> Artificial Sequence

 <220>
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<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

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cacaaaacaa aatacgatat ggaagaccgc ctccatgagg atgaagattc a 51

<210> 11
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 11
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<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
gaatcaatgt tccgtatact gccgctac 28

<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 13
gtagcggcag tatacggaac attgattc 28

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

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<223> PCR primer

<400> 14

gttcctacct ttgttgtaga cgcaccaggc g

31

<210> 15

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> pcr primer

<400> 15

cgcttggtgc gtgtacaaca aaggtaggaa c

31

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<220>

<221> misc_feature

<222> (1)..(23)

<223> y is t/u or c; s is g or c; b is g, c or t/u.

<400> 16

ttyatyggby tsaggbaayat ggg

23

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<220>

<221> misc_feature

<222> (1)..(20)

<223> y is t/u or c; s is g or c; b is g, c or t/u; w is a or t/u; n is
a, c, g or t/u.

<400> 17

gaygcncng tbwssggbgg

20

<210> 18

<211> 21

<212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<220>
 <221> misc_feature
 <222> (1)..(21)
 <223> y is t/u or c; r is g or a; n is a, c, g or t/u.

<400> 18
 catrttrtr caratyttnng c 21

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 19
 gggtttacgag ggcgagaacg gcttgct 27

<210> 20
 <211> 1416
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1416)
 <223>

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 atg aaa aac aaa tgg tat aaa ccg aaa cgg cat tgg aag gag atc gag 48
 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
 1 5 10 15

tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
 20 25 30

ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
 35 40 45

ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192
 Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
 50 55 60

ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240

Pro 65	Leu	Asn	Ile	Thr	Pro 70	Tyr	Tyr	Ala	Ser	Leu 75	Met	Asp	Pro	Asp	Asn 80	
ccg	aga	tgc	ccg	gta	cgc	atg	cag	tct	gtg	ccg	ctt	tct	gaa	gaa	atg	288
Pro	Arg	Cys	Pro	Val	Arg	Met	Gln	Ser	Val	Pro	Leu	Ser	Glu	Glu	Met	
				85					90					95		
cac	aaa	aca	aaa	tac	gat	atg	gaa	gac	ccg	ctt	cat	gag	gat	gaa	gat	336
His	Lys	Thr	Lys	Tyr	Asp	Met	Glu	Asp	Pro	Leu	His	Glu	Asp	Glu	Asp	
			100					105					110			
tca	ccg	gta	ccc	ggt	ctg	aca	cac	cgc	tat	ccc	gac	cg	gtg	ctg	ttt	384
Ser	Pro	Val	Pro	Gly	Leu	Thr	His	Arg	Tyr	Pro	Asp	Arg	Val	Leu	Phe	
		115					120					125				
ctt	gtc	acg	aat	caa	tgt	tcc	gtg	tac	tgc	cg	tac	tgc	aca	aga	agg	432
Leu	Val	Thr	Asn	Gln	Cys	Ser	Val	Tyr	Cys	Arg	Tyr	Cys	Thr	Arg	Arg	
		130				135					140					
cg	ttt	tcc	gga	caa	atc	gga	atg	ggc	gtc	ccc	aaa	aaa	cag	ctt	gat	480
Arg	Phe	Ser	Gly	Gln	Ile	Gly	Met	Gly	Val	Pro	Lys	Lys	Gln	Leu	Asp	
145					150					155					160	
gct	gca	att	gct	tat	atc	cg	gaa	aca	ccc	gaa	atc	cg	gat	tgt	tta	528
Ala	Ala	Ile	Ala	Tyr	Ile	Arg	Glu	Thr	Pro	Glu	Ile	Arg	Asp	Cys	Leu	
				165					170					175		
att	tca	ggc	ggt	gat	ggg	ctg	ctc	atc	aac	gac	caa	att	tta	gaa	tat	576
Ile	Ser	Gly	Gly	Asp	Gly	Leu	Leu	Ile	Asn	Asp	Gln	Ile	Leu	Glu	Tyr	
			180					185					190			
att	tta	aaa	gag	ctg	cg	agc	att	ccg	cat	ctg	gaa	gtc	atc	aga	atc	624
Ile	Leu	Lys	Glu	Leu	Arg	Ser	Ile	Pro	His	Leu	Glu	Val	Ile	Arg	Ile	
		195					200					205				
gga	aca	aga	gct	ccc	gtc	gtc	ttt	ccg	cag	cg	att	acc	gat	cat	ctg	672
Gly	Thr	Arg	Ala	Pro	Val	Val	Phe	Pro	Gln	Arg	Ile	Thr	Asp	His	Leu	
		210				215						220				
tgc	gag	ata	ttg	aaa	aaa	tat	cat	ccg	gtc	tgg	ctg	aac	acc	cat	ttt	720
Cys	Glu	Ile	Leu	Lys	Lys	Tyr	His	Pro	Val	Trp	Leu	Asn	Thr	His	Phe	
225					230					235					240	
aac	aca	agc	atc	gaa	atg	aca	gaa	gaa	tcc	gtt	gag	gca	tgt	gaa	aag	768
Asn	Thr	Ser	Ile	Glu	Met	Thr	Glu	Glu	Ser	Val	Glu	Ala	Cys	Glu	Lys	
				245					250					255		
ctg	gtg	aac	gcg	gga	gtg	ccg	gtc	gga	aat	cag	gct	gtc	gta	tta	gca	816
Leu	Val	Asn	Ala	Gly	Val	Pro	Val	Gly	Asn	Gln	Ala	Val	Val	Leu	Ala	
			260					265					270			
ggt	att	aat	gat	tcg	gtt	cca	att	atg	aaa	aag	ctc	atg	cat	gac	ttg	864
Gly	Ile	Asn	Asp	Ser	Val	Pro	Ile	Met	Lys	Lys	Leu	Met	His	Asp	Leu	
		275				280						285				
gta	aaa	atc	aga	gtc	cg	cct	tat	tat	att	tac	caa	tgt	gat	ctg	tca	912
Val	Lys	Ile	Arg	Val	Arg	Pro	Tyr	Tyr	Ile	Tyr	Gln	Cys	Asp	Leu	Ser	

290	295	300	
gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc			960
Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile			
305	310	315	320
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt			1008
Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe			
	325	330	335
gtc gtt cac gca cca ggc gga gga ggt aaa atc gcc ctg cag ccg aac			1056
Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn			
	340	345	350
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa			1104
Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu			
	355	360	365
ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag			1152
Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln			
	370	375	380
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag			1200
Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys			
	385	390	400
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt			1248
Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe			
	405	410	415
aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca			1296
Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala			
	420	425	430
aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag			1344
Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln			
	435	440	445
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act			1392
Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr			
	450	455	460
gaa tgc gga ggg gat tct tca tga			1416
Glu Cys Gly Gly Asp Ser Ser			
465	470		
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<211> 471			
<212> PRT			
<213> Bacillus subtilis			
<400> 21			
Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu			
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Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
85 90 95

His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp
100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
115 120 125

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg
130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
 245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
 260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
 275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
 290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
 305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
 325 330 335

Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn
 340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
 355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
 370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
 385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
 405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
 420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
 435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
 450 455 460

Glu Cys Gly Gly Asp Ser Ser

465

470

<210> 22
 <211> 438
 <212> DNA
 <213> Clostridium propionicum

<220>
 <221> CDS
 <222> (1)..(438)
 <223>

<400> 22
 atg gta ggt aaa aag gtt gta cat cat tta atg atg agc gca aaa gat 48
 Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp
 1 5 10 15
 gct cac tat act gga aac tta gta aac ggc gct aga att gtg aat cag 96
 Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
 20 25 30
 tgg ggc gac gtt ggt aca gaa tta atg gtt tat gtt gat ggt gac ata 144
 Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
 35 40 45
 agc tta ttc ttg ggc tac aaa gat atc gaa ttc aca gct cct gta tat 192
 Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr
 50 55 60
 gtt ggt gac ttt atg gaa tac cac ggc tgg att gaa aaa gtt ggt aac 240
 Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
 65 70 75 80
 cag tcc tat aca tgt aaa ttt gaa gca tgg aaa gtt gca aca atg gtt 288
 Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Thr Met Val
 85 90 95
 gat atc aca aat cct cag gat aca cgc gca aca gct tgt gag cct ccg 336
 Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
 100 105 110
 gta ttg tgc gga aga gca acg ggt agt ttg ttc atc gca aaa aaa gat 384
 Val Leu Cys Gly Arg Ala Thr Gly Ser Leu Phe Ile Ala Lys Lys Asp
 115 120 125
 cag aga ggc cct cag gaa tcc tct ttt aaa gag aga aag cac ccc ggt 432
 Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Glu Arg Lys His Pro Gly
 130 135 140
 gaa tga 438
 Glu
 145

<210> 23

<211> 145
 <212> PRT
 <213> Clostridium propionicum

<400> 23

Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp
 1 5 10 15

Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
 20 25 30

Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
 35 40 45

Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr
 50 55 60

Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
 65 70 75 80

Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Thr Met Val
 85 90 95

Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
 100 105 110

Val Leu Cys Gly Arg Ala Thr Gly Ser Leu Phe Ile Ala Lys Lys Asp
 115 120 125

Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Glu Arg Lys His Pro Gly
 130 135 140

Glu
 145

<210> 24
 <211> 1554
 <212> DNA
 <213> Megaspheera elsdanii

<220>
 <221> CDS
 <222> (1)..(1554)
 <223>

<400> 24

atg aga aaa gta gaa atc att aca gct gaa caa gca gct cag ctc gta	48
Met Arg Lys Val Glu Ile Ile Thr Ala Glu Gln Ala Ala Gln Leu Val	
1 5 10 15	
aaa gac aac gac acg att acg tct atc ggc ttt gtc agc agc gcc cat	96
Lys Asp Asn Asp Thr Ile Thr Ser Ile Gly Phe Val Ser Ser Ala His	
20 25 30	
ccg gaa gca ctg acc aaa gct ttg gaa aaa cgg ttc ctg gac acg aac	144
Pro Glu Ala Leu Thr Lys Ala Leu Glu Lys Arg Phe Leu Asp Thr Asn	
35 40 45	
acc ccg cag aac ttg acc tac atc tat gca ggc tct cag ggc aaa cgc	192
Thr Pro Gln Asn Leu Thr Tyr Ile Tyr Ala Gly Ser Gln Gly Lys Arg	
50 55 60	
gat ggc cgt gcc gct gaa cat ctg gca cac aca ggc ctt ttg aaa cgc	240
Asp Gly Arg Ala Ala Glu His Leu Ala His Thr Gly Leu Leu Lys Arg	
65 70 75 80	
gcc atc atc ggt cac tgg cag act gta ccg gct atc ggt aaa ctg gct	288
Ala Ile Ile Gly His Trp Gln Thr Val Pro Ala Ile Gly Lys Leu Ala	
85 90 95	
gtc gaa aac aag att gaa gct tac aac ttc tcg cag ggc acg ttg gtc	336
Val Glu Asn Lys Ile Glu Ala Tyr Asn Phe Ser Gln Gly Thr Leu Val	
100 105 110	
cac tgg ttc cgc gcc ttg gca ggt cat aag ctc ggc gtc ttc acc gac	384
His Trp Phe Arg Ala Leu Ala Gly His Lys Leu Gly Val Phe Thr Asp	
115 120 125	
atc ggt ctg gaa act ttc ctc gat ccc cgt cag ctc ggc ggc aag ctc	432
Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu	
130 135 140	
aat gac gta acc aaa gaa gac ctc gtc aaa ctg atc gaa gtc gat ggt	480
Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly	
145 150 155 160	
cat gaa cag ctt ttc tac ccg acc ttc ccg gtc aac gta gct ttc ctc	528
His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu	
165 170 175	
cgc ggt acg tat gct gat gaa tcc ggc aat atc acc atg gac gaa gaa	576
Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu	
180 185 190	
atc ggg cct ttc gaa agc act tcc gta gcc cag gcc gtt cac aac tgt	624
Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys	
195 200 205	
ggc ggt aaa gtc gtc gtc cag gtc aaa gac gtc gtc gct cac ggc agc	672
Gly Gly Lys Val Val Val Gln Val Lys Asp Val Val Ala His Gly Ser	
210 215 220	

ctc gac ccg cgc atg gtc aag atc cct ggc atc tat gtc gac tac gtc	720
Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val	
225 230 235 240	
gtc gta gca gct ccg gaa gac cat cag cag acg tat gac tgc gaa tac	768
Val Val Ala Ala Pro Glu Asp His Gln Gln Thr Tyr Asp Cys Glu Tyr	
245 250 255	
gat ccg tcc ctc agc ggt gaa cat cgt gct cct gaa ggc gct acc gat	816
Asp Pro Ser Leu Ser Gly Glu His Arg Ala Pro Glu Gly Ala Thr Asp	
260 265 270	
gca gct ctc ccc atg agc gct aag aaa atc atc ggc cgc cgc ggc gct	864
Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala	
275 280 285	
ttg gaa ttg act gaa aac gct gtc gtc aac ctc ggc gtc ggt gct ccg	912
Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro	
290 295 300	
gaa tac gtt gct tct gtt gcc ggt gaa gaa ggt atc gcc gat acc att	960
Glu Tyr Val Ala Ser Val Ala Gly Glu Glu Gly Ile Ala Asp Thr Ile	
305 310 315 320	
acc ctg acc gtc gaa ggt ggc gcc atc ggt ggc gta ccg cag ggc ggt	1008
Thr Leu Thr Val Glu Gly Gly Ala Ile Gly Gly Val Pro Gln Gly Gly	
325 330 335	
gcc cgc ttc ggt tgc tcc cgc aat gcc gat gcc atc atc gac cac acc	1056
Ala Arg Phe Gly Ser Ser Arg Asn Ala Asp Ala Ile Ile Asp His Thr	
340 345 350	
tat cag ttc gac ttc tac gat ggc ggc ggt ctg gac atc gct tac ctc	1104
Tyr Gln Phe Asp Phe Tyr Asp Gly Gly Gly Leu Asp Ile Ala Tyr Leu	
355 360 365	
ggc ctg gcc cag tgc gat ggc tgc ggc aac atc aac gtc agc aag ttc	1152
Gly Leu Ala Gln Cys Asp Gly Ser Gly Asn Ile Asn Val Ser Lys Phe	
370 375 380	
ggt act aac gtt gcc ggc tgc ggc ggt ttc ccc aac att tcc cag cag	1200
Gly Thr Asn Val Ala Gly Cys Gly Gly Phe Pro Asn Ile Ser Gln Gln	
385 390 395 400	
aca ccg aat gtt tac ttc tgc ggc acc ttc acg gct ggc ggc ttg aaa	1248
Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys	
405 410 415	
atc gct gtc gaa gac ggc aaa gtc aag atc ctc cag gaa ggc aaa gcc	1296
Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala	
420 425 430	
aag aag ttc atc aaa gct gtc gac cag atc act ttc aac ggt tcc tat	1344
Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr	
435 440 445	
gca gcc cgc aac ggc aaa cac gtt ctc tac atc aca gaa cgc tgc gta	1392

Ala	Ala	Arg	Asn	Gly	Lys	His	Val	Leu	Tyr	Ile	Thr	Glu	Arg	Cys	Val	
450						455					460					
ttt	gaa	ctg	acc	aaa	gaa	ggc	ttg	aaa	ctc	atc	gaa	gtc	gca	ccg	ggc	1440
Phe	Glu	Leu	Thr	Lys	Glu	Gly	Leu	Lys	Leu	Ile	Glu	Val	Ala	Pro	Gly	
465					470				475						480	
atc	gat	att	gaa	aaa	gat	atc	ctc	gct	cac	atg	gac	ttc	aag	ccg	atc	1488
Ile	Asp	Ile	Glu	Lys	Asp	Ile	Leu	Ala	His	Met	Asp	Phe	Lys	Pro	Ile	
				485				490						495		
att	gat	aat	ccg	aaa	ctc	atg	gat	gcc	cgc	ctc	ttc	cag	gac	ggc	ccc	1536
Ile	Asp	Asn	Pro	Lys	Leu	Met	Asp	Ala	Arg	Leu	Phe	Gln	Asp	Gly	Pro	
			500					505					510			
atg	gga	ctg	aaa	aaa	taa											1554
Met	Gly	Leu	Lys	Lys												
				515												

<210> 25
 <211> 517
 <212> PRT
 <213> Megasphaera elsdenii

<400> 25

Met	Arg	Lys	Val	Glu	Ile	Ile	Thr	Ala	Glu	Gln	Ala	Ala	Gln	Leu	Val	
1				5					10					15		
Lys	Asp	Asn	Asp	Thr	Ile	Thr	Ser	Ile	Gly	Phe	Val	Ser	Ser	Ala	His	
			20					25					30			
Pro	Glu	Ala	Leu	Thr	Lys	Ala	Leu	Glu	Lys	Arg	Phe	Leu	Asp	Thr	Asn	
		35					40					45				
Thr	Pro	Gln	Asn	Leu	Thr	Tyr	Ile	Tyr	Ala	Gly	Ser	Gln	Gly	Lys	Arg	
	50					55					60					
Asp	Gly	Arg	Ala	Ala	Glu	His	Leu	Ala	His	Thr	Gly	Leu	Leu	Lys	Arg	
65					70				75						80	
Ala	Ile	Ile	Gly	His	Trp	Gln	Thr	Val	Pro	Ala	Ile	Gly	Lys	Leu	Ala	
				85					90					95		
Val	Glu	Asn	Lys	Ile	Glu	Ala	Tyr	Asn	Phe	Ser	Gln	Gly	Thr	Leu	Val	
			100					105					110			
His	Trp	Phe	Arg	Ala	Leu	Ala	Gly	His	Lys	Leu	Gly	Val	Phe	Thr	Asp	
		115					120					125				

Ile Gly Leu Glu Thr Phe Leu Asp Pro Arg Gln Leu Gly Gly Lys Leu
130 135 140

Asn Asp Val Thr Lys Glu Asp Leu Val Lys Leu Ile Glu Val Asp Gly
145 150 155 160

His Glu Gln Leu Phe Tyr Pro Thr Phe Pro Val Asn Val Ala Phe Leu
165 170 175

Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Met Asp Glu Glu
180 185 190

Ile Gly Pro Phe Glu Ser Thr Ser Val Ala Gln Ala Val His Asn Cys
195 200 205

Gly Gly Lys Val Val Val Gln Val Lys Asp Val Val Ala His Gly Ser
210 215 220

Leu Asp Pro Arg Met Val Lys Ile Pro Gly Ile Tyr Val Asp Tyr Val
225 230 235 240

Val Val Ala Ala Pro Glu Asp His Gln Gln Thr Tyr Asp Cys Glu Tyr
245 250 255

Asp Pro Ser Leu Ser Gly Glu His Arg Ala Pro Glu Gly Ala Thr Asp
260 265 270

Ala Ala Leu Pro Met Ser Ala Lys Lys Ile Ile Gly Arg Arg Gly Ala
275 280 285

Leu Glu Leu Thr Glu Asn Ala Val Val Asn Leu Gly Val Gly Ala Pro
290 295 300

Glu Tyr Val Ala Ser Val Ala Gly Glu Glu Gly Ile Ala Asp Thr Ile
305 310 315 320

Thr Leu Thr Val Glu Gly Gly Ala Ile Gly Gly Val Pro Gln Gly Gly
325 330 335

Ala Arg Phe Gly Ser Ser Arg Asn Ala Asp Ala Ile Ile Asp His Thr
340 345 350

Tyr Gln Phe Asp Phe Tyr Asp Gly Gly Gly Leu Asp Ile Ala Tyr Leu
 355 360 365

Gly Leu Ala Gln Cys Asp Gly Ser Gly Asn Ile Asn Val Ser Lys Phe
 370 375 380

Gly Thr Asn Val Ala Gly Cys Gly Gly Phe Pro Asn Ile Ser Gln Gln
 385 390 395 400

Thr Pro Asn Val Tyr Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys
 405 410 415

Ile Ala Val Glu Asp Gly Lys Val Lys Ile Leu Gln Glu Gly Lys Ala
 420 425 430

Lys Lys Phe Ile Lys Ala Val Asp Gln Ile Thr Phe Asn Gly Ser Tyr
 435 440 445

Ala Ala Arg Asn Gly Lys His Val Leu Tyr Ile Thr Glu Arg Cys Val
 450 455 460

Phe Glu Leu Thr Lys Glu Gly Leu Lys Leu Ile Glu Val Ala Pro Gly
 465 470 475 480

Ile Asp Ile Glu Lys Asp Ile Leu Ala His Met Asp Phe Lys Pro Ile
 485 490 495

Ile Asp Asn Pro Lys Leu Met Asp Ala Arg Leu Phe Gln Asp Gly Pro
 500 505 510

Met Gly Leu Lys Lys
 515

<210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 26
 caagctgggt ctgttcacgc tggatg

<210> 27
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 27
 aagcggttct cgccctcgta aacctga

27

<210> 28
 <211> 416
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 28

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
 1 5 10 15

Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
 20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly
 35 40 45

Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
 50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
 65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
 85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
 100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
 115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
 130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
 145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly
325 330 335

Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
 385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
 405 410 415

<210> 29
 <211> 1251
 <212> DNA
 <213> Porphyromonas gingivalis

<220>
 <221> CDS
 <222> (1)..(1251)
 <223>

<400> 29
 atg gca gaa agt cgt aga aag tat tat ttc cct gat gtc acc gat gag 48
 Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
 1 5 10 15
 caa tgg tac gac tgg cat tgg cag gtc ctc aat cga att gag acg ctc 96
 Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
 20 25 30
 gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gaa gag gga 144
 Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly
 35 40 45
 gta aaa gaa tcg ccc aaa gta ctc cga atg gct atc aca cct tat tat 192
 Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
 50 55 60
 ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa 240
 Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
 65 70 75 80
 gcc att cct act caa cag gaa ctg gta cgt gct cct gaa gat cag gta 288
 Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
 85 90 95
 gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat 336
 Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
 100 105 110
 cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg 384
 Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
 115 120 125
 tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct 432
 Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
 130 135 140

tct tct cct tct gag cgc atc gat cga tgc att gac tat ata gcc aat	480
Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn	
145 150 155 160	
aca ccg aca gtc cgc gat gtt ttg cta tgc gga ggc gat gcc ctc ctt	528
Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu	
165 170 175	
gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata	576
Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile	
180 185 190	
cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctc	624
Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu	
195 200 205	
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat	672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His	
210 215 220	
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa	720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu	
225 230 235 240	
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg	768
Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu	
245 250 255	
ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg	816
Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val	
260 265 270	
atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac	864
Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr	
275 280 285	
tat ata tat gta tgc gat ctt tgc ctt gga ata ggt cat ttc cgc acg	912
Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr	
290 295 300	
ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc	960
Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr	
305 310 315 320	
tgc ggc tat gca gtt cct acc ttt gtg gta ggt gct ccg ggg ggt ggt	1008
Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly	
325 330 335	
ggt aag ata cct gta acg ccg aac tat gtt gta tct cag tcc cca cga	1056
Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg	
340 345 350	
cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag	1104
His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu	
355 360 365	
ccg gag aat tat cat gag gag tgc gat tgt gag gac tgt cga gcc ggt	1152

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
 370 375 380

aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct 1200
 Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
 385 390 395 400

atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac 1248
 Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
 405 410 415

tga 1251

<210> 30
 <211> 416
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 30

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
 1 5 10 15

Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
 20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly
 35 40 45

Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
 50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
 65 70 75 80

Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
 85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
 100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
 115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
 130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
 145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
 165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
 180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
 195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
 210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
 225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
 245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
 260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
 275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
 290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr
 305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly
 325 330 335

Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
 340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
 355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly

370

375

380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
 385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
 405 410 415

<210> 31

<211> 471

<212> PRT

<213> Bacillus subtilis

<400> 31

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
 1 5 10 15

Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
 20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
 35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
 85 90 95

His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp
 100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
 115 120 125

Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg
 130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
 145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val Asp Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
 385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
 405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
 420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
 435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
 450 455 460

Glu Cys Gly Gly Asp Ser Ser
 465 470

<210> 32
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 32
 cg catt caag tca aag acgt tc agg cta

28

<210> 33
 <211> 1387
 <212> DNA
 <213> *Alcaligenes faecalis*

<220>
 <221> CDS
 <222> (408)..(1304)
 <223>

<400> 33
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 gcaaaccttc gccaaagggtg cgcctgggttc ggctcgtttg tcctttgagc tgctggagag 120
 ggtgcatcac ctgtcttttg ccgatgtttt ccgtctggaa tacatttgtt cgctgcaatg 180
 tggcgtagac ggcgacttcc aggaaggcat acgggcactg ctgattgata aagacaaaca 240
 gccgcgctgg aatcctgcct cgctggaaca ggcggatgca cgctgggttg aacgtttttt 300

tggtcctgcc tggccggcag aaacgactca tcccttggct gacctgtaac ccaggcagac	360
cgctgcggcg ccagacggcg ccgctttcat aatgacgagg agacaaa atg agt aac	416
Met Ser Asn	
1	
acg att gca ttt atc ggg ctg ggc cat atg ggt aaa ccc atg gcg ctg	464
Thr Ile Ala Phe Ile Gly Leu Gly His Met Gly Lys Pro Met Ala Leu	
5 10 15	
aat ctg ctc aaa gcc ggt cat agc ctg aac gtc ttt gac ttg aat gcg	512
Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp Leu Asn Ala	
20 25 30 35	
caa gcc atg cag gaa ctg cag gca gca ggg gca cag gtg ggg gaa tcg	560
Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val Gly Glu Ser	
40 45 50	
gcg gtg caa atc gcc caa gac gcg cag atg gtc ttt acc atg ctg cct	608
Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr Met Leu Pro	
55 60 65	
gct ggc cgc cat gtt cgt cag gtt tac gag ggc gag aac ggc ttg ctg	656
Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn Gly Leu Leu	
70 75 80	
cag act gtg gcc ccc ggt acg gtg ctg gtc gat tgc agc acc att gat	704
Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser Thr Ile Asp	
85 90 95	
gcg caa acc agc cag gat ctg gcg gcc aaa gcc agc aag ctg ggt ctg	752
Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys Leu Gly Leu	
100 105 110 115	
ttc atg ctg gat gcg ccg gtc tcc ggt ggg acc ggt ggc gcc att gct	800
Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly Ala Ile Ala	
120 125 130	
ggc acc ttg acc ttt atg gtc ggg ggc gag gat cag gcc ctg gaa aag	848
Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala Leu Glu Lys	
135 140 145	
gcg cgc cct tac ttg gat gcc atg ggc aag aac att ttc cac gcg ggt	896
Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe His Ala Gly	
150 155 160	
aaa gcc ggt gcg ggt cag gtt gcc aag att tgc aac aat atg ctc ttg	944
Lys Ala Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn Met Leu Leu	
165 170 175	
ggg att ttg atg gcg ggt act gct gaa gcc ttg gct ttg ggc gtt gcc	992
Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu Gly Val Ala	
180 185 190 195	
cac ggt ctg gac cct gcc gtg ctg tcg acc atc atg gcg cgc agt tcc	1040
His Gly Leu Asp Pro Ala Val Leu Ser Thr Ile Met Ala Arg Ser Ser	

200	205	210	
ggt cga aac tgg gca acc gag ctg tac aac ccc tgg cct ggg gtg atg			1088
Gly Arg Asn Trp Ala Thr Glu Leu Tyr Asn Pro Trp Pro Gly Val Met			
215	220	225	
ccg gat gta ccg gct tcg cgt gat tat cag ggc ggt ttt gcg acg ggc			1136
Pro Asp Val Pro Ala Ser Arg Asp Tyr Gln Gly Gly Phe Ala Thr Gly			
230	235	240	
ctg atg ctc aaa gac ctg ggt ctg gca gcc gat gcg gct gtc agc cag			1184
Leu Met Leu Lys Asp Leu Gly Leu Ala Ala Asp Ala Ala Val Ser Gln			
245	250	255	
aac agc gcg acg cct ttg ggc gaa ctg gca cgt aac ctg ttc gcc ttg			1232
Asn Ser Ala Thr Pro Leu Gly Glu Leu Ala Arg Asn Leu Phe Ala Leu			
260	265	270	275
cac gcc gca caa ggt cag aat gca ggg ctg gat ttc tcc agc att ctt			1280
His Ala Ala Gln Gly Gln Asn Ala Gly Leu Asp Phe Ser Ser Ile Leu			
280	285	290	
aat ttg tac cgt cag aag cac taa gttctggcag tgcgtagggc aggggctgca			1334
Asn Leu Tyr Arg Gln Lys His			
295			
gttcacagcgc ctgtccttgc tccaattgaa actggccttg ttccaggtcc gcc			1387

<210> 34
 <211> 298
 <212> PRT
 <213> *Alcaligenes faecalis*

<400> 34

Met Ser Asn Thr Ile Ala Phe Ile Gly Leu Gly His Met Gly Lys Pro
1 5 10 15

Met Ala Leu Asn Leu Leu Lys Ala Gly His Ser Leu Asn Val Phe Asp
20 25 30

Leu Asn Ala Gln Ala Met Gln Glu Leu Gln Ala Ala Gly Ala Gln Val
35 40 45

Gly Glu Ser Ala Val Gln Ile Ala Gln Asp Ala Gln Met Val Phe Thr
50 55 60

Met Leu Pro Ala Gly Arg His Val Arg Gln Val Tyr Glu Gly Glu Asn
65 70 75 80

Gly Leu Leu Gln Thr Val Ala Pro Gly Thr Val Leu Val Asp Cys Ser

85

90

95

Thr Ile Asp Ala Gln Thr Ser Gln Asp Leu Ala Ala Lys Ala Ser Lys
 100 105 110

Leu Gly Leu Phe Met Leu Asp Ala Pro Val Ser Gly Gly Thr Gly Gly
 115 120 125

Ala Ile Ala Gly Thr Leu Thr Phe Met Val Gly Gly Glu Asp Gln Ala
 130 135 140

Leu Glu Lys Ala Arg Pro Tyr Leu Asp Ala Met Gly Lys Asn Ile Phe
 145 150 155 160

His Ala Gly Lys Ala Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn
 165 170 175

Met Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu
 180 185 190

Gly Val Ala His Gly Leu Asp Pro Ala Val Leu Ser Thr Ile Met Ala
 195 200 205

Arg Ser Ser Gly Arg Asn Trp Ala Thr Glu Leu Tyr Asn Pro Trp Pro
 210 215 220

Gly Val Met Pro Asp Val Pro Ala Ser Arg Asp Tyr Gln Gly Gly Phe
 225 230 235 240

Ala Thr Gly Leu Met Leu Lys Asp Leu Gly Leu Ala Ala Asp Ala Ala
 245 250 255

Val Ser Gln Asn Ser Ala Thr Pro Leu Gly Glu Leu Ala Arg Asn Leu
 260 265 270

Phe Ala Leu His Ala Ala Gln Gly Gln Asn Ala Gly Leu Asp Phe Ser
 275 280 285

Ser Ile Leu Asn Leu Tyr Arg Gln Lys His
 290 295

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 <220>
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 agagagcata tgtctttttca ccttcggc 28

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 <210> 43
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 <220>
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 <210> 44
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<400> 44
cgacggatcc tcaacgacca ctgaagttgg 30

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<210> 47
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<400> 47
ctagtctaga ggaaaccgct taacgaactc 30

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<210> 49
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<220>
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<400> 50
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<220>
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<210> 52
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<400> 52
 cgacggatcc gcagtgagtg agccttgag 30

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<220>
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<400> 53
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 Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp

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gct cac tat act gga aac tta gta aac ggc gct aga atc gtg aat cag				96
Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln				
	20	25	30	
tgg ggc gac gta ggt aca gaa tta atg gtt tat gtt gat ggt gac atc				144
Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile				
	35	40	45	
agc tta ttc ttg ggc tac aaa gat atc gaa ttc aca gct cct gta tat				192
Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr				
	50	55	60	
ggt ggt gat ttt atg gaa tac cac ggc tgg att gaa aaa gtt ggc aac				240
Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn				
	65	70	75	80
cag tcc tat aca tgt aaa ttt gaa gca tgg aaa gta gca aag atg gtt				288
Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Lys Met Val				
	85	90	95	
gat atc aca aat cca cag gat aca cgt gca aca gct tgt gaa cct ccg				336
Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro				
	100	105	110	
gta ctt tgt ggt act gca aca ggc agc ctt ttc atc gca aag gat aat				384
Val Leu Cys Gly Thr Ala Thr Gly Ser Leu Phe Ile Ala Lys Asp Asn				
	115	120	125	
cag aga ggt cct cag gaa tct tcc ttc aag gat gca aag cac cct caa				432
Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Asp Ala Lys His Pro Gln				
	130	135	140	
taa				435

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Met Val Gly Lys Lys Val Val His His Leu Met Met Ser Ala Lys Asp
1 5 10 15

Ala His Tyr Thr Gly Asn Leu Val Asn Gly Ala Arg Ile Val Asn Gln
20 25 30

Trp Gly Asp Val Gly Thr Glu Leu Met Val Tyr Val Asp Gly Asp Ile
35 40 45

Ser Leu Phe Leu Gly Tyr Lys Asp Ile Glu Phe Thr Ala Pro Val Tyr

50

55

60

Val Gly Asp Phe Met Glu Tyr His Gly Trp Ile Glu Lys Val Gly Asn
65 70 75 80

Gln Ser Tyr Thr Cys Lys Phe Glu Ala Trp Lys Val Ala Lys Met Val
85 90 95

Asp Ile Thr Asn Pro Gln Asp Thr Arg Ala Thr Ala Cys Glu Pro Pro
100 105 110

Val Leu Cys Gly Thr Ala Thr Gly Ser Leu Phe Ile Ala Lys Asp Asn
115 120 125

Gln Arg Gly Pro Gln Glu Ser Ser Phe Lys Asp Ala Lys His Pro Gln
130 135 140

<210> 55
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<210> 56
<211> 30
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<220>
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<400> 56
ctagtctaga tcaacgacca ctgaagttgg 30

<210> 57
<211> 40
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<220>
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<400> 57
aaggaaaaaa gcggccgctt taatatgcga tttggaggag 40

<210> 58
 <211> 30
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 <400> 58
 ctagtctaga gcagtgagtg agccttggag 30

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 <400> 59
 cacacagaat tcattaaaga ggag 24

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 cataatcaaa ctcaaagtca accatataag atctcctcct tacttcatga agaatcccct 60
 cc 62

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 ggaggggatt cttcatgaag taaggaggag atcttatatg gttgactttg agtttgatta 60
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cgtgttactc attttgtctc ctcgtcattt acttgaagtc tgctaagata c 51

<210> 63

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